

SEULBERGER et al., Serial No. 09/462,629

specification and substitute replacement pages 28-32 attached hereto as separate pages.

REMARKS

A copy of the corrected Sequence Listing in computer readable form is attached hereto. The content of the paper copy of the Sequence Listing and the copy of the Sequence Listing in computer readable form is the same, and includes no new matter.

It is believed that by submitting the present amendment and sequence listing diskette, the application now fully complies with the requirements of 37 CFR 1.821-1.825. Favorable action by the examiner is solicited.

Please charge any shortage in fees due in connection with the filing of this paper, including Extension of Time fees to Deposit Account No. 11.0345. Please credit any excess fees to such deposit account.

Respectfully submitted,

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HBK/DSK/kas



SEQUENCE LISTING

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<110> Seulberger, Harald
 Leichl, Jenms
 Schmidt, Ralf-Michael
 Krupinska, Karin
 Falk, Jon

<120> DNA sequence encoding a hydroxyphenylpyruvate dioxygenase, and its overproduction in plants

<140> US 09/462,629

<141> 2000-01-11

<150> PCT/EP98/03832

<151> 1998-06-23

<160> 2

<170> WordPerfect version 6.1

<210> 1

<211> 1565

<212> DNA

<213> hppd from barley

<220>

<221> CDS

<222> 9 ... 1313

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Ala Ala Val Thr Pro Glu His Ala Arg Pro His Arg Met Val Arg Phe	
15 20 25 30	
aac ccg cgc agc gac cgc ttc cac acg ctc tcc ttc cac cac gtc gag	146
Asn Pro Arg Ser Asp Arg Phe His Thr Leu Ser Phe His His Val Glu	
35 40 45	
ttc tgg tgc gcg gac gcc gcc tcc gcc gcc ggc cgc ttc gcg ttc gcg	194
Phe Trp Cys Ala Asp Ala Ala Ser Ala Ala Gly Arg Phe Ala Phe Ala	
50 55 60	
ctc ggc gcg ccg ctc gcc gcc agg tcc gac ctc tcc acg ggg aac tcc	242
Leu Gly Ala Pro Leu Ala Ala Arg Ser Asp Leu Ser Thr Gly Asn Ser	
65 70 75	
gcg cac gcc tcc cag ctg ctc cgc tcg ggc tcc ctc gcc ttc ctc ttc	290

Ala His Ala Ser Gln Leu Leu Arg Ser Gly Ser Leu Ala Phe Leu Phe	
80 85 90	
acc gcg ccc tac gcc aac ggc tgc gac gcc gcc acc gcc tcc ctg ccc	338
Thr Ala Pro Tyr Ala Asn Gly Cys Asp Ala Ala Thr Ala Ser Leu Pro	
95 100 105 110	
tcc ttc tcc gcc gac gcc gcg cgc cgg ttc tcc gcc gac cac ggg atc	386
Ser Phe Ser Ala Asp Ala Ala Arg Arg Phe Ser Ala Asp His Gly Ile	
115 120 125	
gcg gtg cgc tcc gta gcg ctg cgc gtc gca gac gcc gcc gag gcc ttc	434
Ala Val Arg Ser Val Ala Leu Arg Val Ala Asp Ala Ala Glu Ala Phe	
130 135 140	
cgc gcc agt cgt cga cgg ggc gcg cgc ccg gcc ttc gcc ccc gtg gac	482
Arg Ala Ser Arg Arg Arg Gly Ala Arg Pro Ala Phe Ala Pro Val Asp	
145 150 155	
ctc ggc cgc ggc ttc gcg ttc gcg gag gtc gag ctc tac ggc gac gtc	530
Leu Gly Arg Gly Phe Ala Phe Ala Glu Val Glu Leu Tyr Gly Asp Val	
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gtg ctc cgc ttc gtc agc cac ccg gac ggc acg gac gtg ccc ttc ttg	578
Val Leu Arg Phe Val Ser His Pro Asp Gly Thr Asp Val Pro Phe Leu	
175 180 185 190	
ccg ggg ttc gag ggc gta acc aac ccg gac gcc gtg gac tac ggc ctg	626
Pro Gly Phe Glu Gly Val Thr Asn Pro Asp Ala Val Asp Tyr Gly Leu	
195 200 205	
acg cgg ttc gac cac gtc gtc ggc aac gtc ccg gag ctt gcc ccc gcc	674
Thr Arg Phe Asp His Val Val Gly Asn Val Pro Glu Leu Ala Pro Ala	
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gca gcc tac atc gcc ggg ttc acg ggg ttc cac gag ttc gcc gag ttc	722
Ala Ala Tyr Ile Ala Gly Phe Thr Gly Phe His Glu Phe Ala Glu Phe	
225 230 235	
acg gcg gag gac gtg ggc acg acc gag agc ggg ctc aac tcg gtg gtg	770
Thr Ala Glu Asp Val Gly Thr Thr Glu Ser Gly Leu Asn Ser Val Val	
240 245 250	
ctc gcc aac aac tcg gag ggc gtg ctg ctg ccg ctc aac gag ccg gtg	818
Leu Ala Asn Asn Ser Glu Gly Val Leu Leu Pro Leu Asn Glu Pro Val	
255 260 265 270	
cac ggc acc aag cgc cgg agc cag ata cag acg ttc ctg gaa cac cac	866
His Gly Thr Lys Arg Arg Ser Gln Ile Gln Thr Phe Leu Glu His His	
275 280 285	
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Gly Gly Pro Gly Val Gln His Ile Ala Val Ala Ser Ser Asp Val Leu	

290	295	300	
agg acg ctc agg aag atg cgt gcg cgc tcc gcc atg ggc ggc ttc gac			962
Arg Thr Leu Arg Lys Met Arg Ala Arg Ser Ala Met Gly Gly Phe Asp			
305	310	315	
ttc ctg cca ccc ccg ctg ccg aag tac tac gaa ggc gtg cga cgc ctt			1010
Phe Leu Pro Pro Pro Leu Pro Lys Tyr Tyr Glu Gly Val Arg Arg Leu			
320	325	330	
gcc ggg gat gtc ctc tcg gag gcg cag atc aag gaa tgc cag gag ctg			1058
Ala Gly Asp Val Leu Ser Glu Ala Gln Ile Lys Glu Cys Gln Glu Leu			
335	340	345	350
ggt gtg ctc gtc gat agg gac gac caa ggg gtg ttg ctc caa atc ttc			1106
Gly Val Leu Val Asp Arg Asp Asp Gln Gly Val Leu Leu Gln Ile Phe			
355	360	365	
acc aag cca gta ggg gac agg ccg acc ttg ttc ctg gag atg atc cag			1154
Thr Lys Pro Val Gly Asp Arg Pro Thr Leu Phe Leu Glu Met Ile Gln			
370	375	380	
agg atc ggg tgc atg gag aag gac gag aga ggg gaa gag tac cag aag			1202
Arg Ile Gly Cys Met Glu Lys Asp Glu Arg Gly Glu Glu Tyr Gln Lys			
385	390	395	
ggt ggc tgc ggc ggg ttc ggc aaa ggc aac ttc tcc gag ctg ttc aag			1250
Gly Gly Cys Gly Gly Phe Gly Lys Gly Asn Phe Ser Glu Leu Phe Lys			
400	405	410	
tcc att gaa gat tac gag aag tcc ctt gaa gcc aag caa tct gct gca			1298
Ser Ile Glu Asp Tyr Glu Lys Ser Leu Glu Ala Lys Gln Ser Ala Ala			
415	420	425	430
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Val Gln Gly Ser			
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gaagctgaag acagatgtat cctatgtatg atgggtgtaa tggatggtag aggggctcac			1470
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<211> 434

<212> PRT

<400> 2

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Cys Ala Asp Ala Ala Ser Ala Ala Gly Arg Phe Ala Phe Ala Leu Gly	50	55	60
Ala Pro Leu Ala Ala Arg Ser Asp Leu Ser Thr Gly Asn Ser Ala His	65	70	75
Ala Ser Gln Leu Leu Arg Ser Gly Ser Leu Ala Phe Leu Phe Thr Ala	85	90	95
Pro Tyr Ala Asn Gly Cys Asp Ala Ala Thr Ala Ser Leu Pro Ser Phe	100	105	110
Ser Ala Asp Ala Ala Arg Arg Phe Ser Ala Asp His Gly Ile Ala Val	115	120	125
Arg Ser Val Ala Leu Arg Val Ala Asp Ala Ala Glu Ala Phe Arg Ala	130	135	140
Ser Arg Arg Arg Gly Ala Arg Pro Ala Phe Ala Pro Val Asp Leu Gly	145	150	155
Arg Gly Phe Ala Phe Ala Glu Val Glu Leu Tyr Gly Asp Val Val Leu	165	170	175
Arg Phe Val Ser His Pro Asp Gly Thr Asp Val Pro Phe Leu Pro Gly	180	185	190
Phe Glu Gly Val Thr Asn Pro Asp Ala Val Asp Tyr Gly Leu Thr Arg	195	200	205
Phe Asp His Val Val Gly Asn Val Pro Glu Leu Ala Pro Ala Ala Ala	210	215	220
Tyr Ile Ala Gly Phe Thr Gly Phe His Glu Phe Ala Glu Phe Thr Ala	225	230	235
Glu Asp Val Gly Thr Thr Glu Ser Gly Leu Asn Ser Val Val Leu Ala	245	250	255
Asn Asn Ser Glu Gly Val Leu Leu Pro Leu Asn Glu Pro Val His Gly	260	265	270
Thr Lys Arg Arg Ser Gln Ile Gln Thr Phe Leu Glu His His Gly Gly	275	280	285

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Pro Gly Val Gln His. Ile Ala Val Ala Ser Ser Asp Val Leu Arg Thr
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Leu Arg Lys Met Arg Ala Arg Ser Ala Met Gly Gly Phe Asp Phe Leu
 305 310 315 320

Pro Pro Pro Leu Pro Lys Tyr Tyr Glu Gly Val Arg Arg Leu Ala Gly
 325 330 335

Asp Val Leu Ser Glu Ala Gln Ile Lys Glu Cys Gln Glu Leu Gly Val
 340 345 350

Leu Val Asp Arg Asp Asp Gln Gly Val Leu Leu Gln Ile Phe Thr Lys
 355 360 365

Pro Val Gly Asp Arg Pro Thr Leu Phe Leu Glu Met Ile Gln Arg Ile
 370 375 380

Gly Cys Met Glu Lys Asp Glu Arg Gly Glu Glu Tyr Gln Lys Gly Gly
 385 390 395 400

Cys Gly Gly Phe Gly Lys Gly Asn Phe Ser Glu Leu Phe Lys Ser Ile
 405 410 415

Glu Asp Tyr Glu Lys Ser Leu Glu Ala Lys Gln Ser Ala Ala Val Gln
 420 425 430

Gly Ser--.